AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

Claims 1-4 (canceled).

Claim 5 (new): A method for detecting a mutation which causes or is associated with long QT syndrome comprising amplifying one of exons 1-15 of HERG with a pair of primers such that the entire exon, and no other exon or portion thereof, is amplified, and analyzing the amplified exon for a mutation which causes or is associated with long QT syndrome.

Claim 6 (new): The method of claim 5, wherein the pair of primers is selected from the group consisting of:

a) SEQ ID NOs:56 and 57;
b) SEQ ID NOs:58 and 59;
c) SEQ ID NOs:60 and 61;
d) SEQ ID NOs:62 and 63;
e) SEQ ID NOs:64 and 65;
f) SEQ ID NOs:66 and 67;
g) SEQ ID NOs:68 and 69;
h) SEQ ID NOs:70 and 71;
i) SEQ ID NOs:76 and 77;
j) SEQ ID NOs:78 and 79;
k) SEQ ID NOs:80 and 81;
l) SEQ ID NOs:82 and 83;
m) SEQ ID NOs:84 and 85;

n) SEQ ID NOs:86 and 87;

o) SEQ ID NOs:88 and 89;

p) SEQ ID NOs:90 and 91;

q) SEQ ID NOs:92 and 93; and

r) SEQ ID NOs:94 and 95.

Claim 7 (new): The method of claim 5, wherein the analyzing step is performed by single-stranded conformation polymorphism technique.

Claim 8 (new): The method of claim 6, wherein the analyzing step is performed by single-stranded conformation polymorphism technique.

Claim 9 (new): The method of claim 5, wherein the analyzing step is performed by sequencing the amplified exon.

Claim 10 (new): The method of claim 6, wherein the analyzing step is performed by sequencing the amplified exon.